CLAIMS

What is claimed is:

1. A method for analyzing microarray analysis quality comprising:

Performing a principal component analysis of a plurality of quality metrics; and

Examining the egenvectors resulted from the principal component analysis.

2. The method of Claim 1 wherein the microarray analysis is gene expression analysis.

3. The method of Claim 2 wherein principal analysis comprises log-transformation of non-normally distributed quality metrics.

4. The method of Claim 3 wherein the quality metrics comprises discrete quality metrics.

5. The method of Claim 4 wherein the quality metrics comprises RNA quality metrics.

6. The method of Claim 4 wherein the quality metrics comprises background metrics.

7. The method of Claim 3 wherein the quality metrics comprises cumulative metrics.

8. The method of Claim 7 wherein the quality metrics comprises in vitro transcription yield.

9. The method of Claim 1 wherein the microarray analysis is a genotyping analysis.

10. The method of Claim 1 wherein the microarray analysis is a resequencing analysis.

11. A method for analyzing microarray analysis quality comprising:

Performing an ANOVA of a microarray quality metrics data; and

Analyzing outliers, wherein the outliers are derived from residuals from the ANOVA.

12. The method of Claim 11 wherein the microarray analysis is a gene expression analysis.

13. The method of Claim 12 wherein principal analysis comprises log-transformation of non-normally distributed quality metrics.

14. The method of Claim 13 wherein the quality metrics comprises discrete quality metrics.

15. The method of Claim 14 wherein the quality metrics comprises RNA quality metrics.

16. The method of Claim 14 wherein the quality metrics comprises background metrics.

17. The method of Claim 13 wherein the quality metrics comprises cumulative metrics.

18. The method of Claim 17 wherein the quality metrics comprises in vitro transcription yield.

19. The method of Claim 11 wherein the microarray analysis is a genotyping analysis.

20. The method of Claim 11 wherein the microarray analysis is a resequencing analysis.